RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/537,971
Source: IFWP
Date Processed by STIC: 11/08/2005

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IFWP

RAW SEQUENCE LISTING DATE: 11/08/2005
PATENT APPLICATION: **US/10/537,971** TIME: 12:18:08

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\11082005\J537971.raw**

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     2 <110> APPLICANT: NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY
     3       JAPAN SCIENCE AND TECHNOLOGY AGENCY
     5 <120> TITLE OF INVENTION: Monitor protein for measuring protein processing
     7 <130> FILE REFERENCE: P03-133
C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/537,971
C--> 8 <141> CURRENT FILING DATE: 2005-06-09
     8 <150> PRIOR APPLICATION NUMBER: JP2002-360744
     9 <151> PRIOR FILING DATE: 2002-12-12
W--> 10 <160> NUMBER OF SEQ ID: 5
    11 <170> SOFTWARE: PatentIn version 3.1
    13 <210> SEQ ID NO: 1
    14 <211> LENGTH: 2502
    15 <212> TYPE: DNA
    16 <213> ORGANISM: mammalian
    18 <400> SEQUENCE: 1
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    21 gcatgtcctg tagaagcgga accgccatca agtacaccaa cagttccaac ttcttgtgaa    120
    23 gctaaagaag gagaatgtat agataccaga tgcgcaacat gtaaacgaga tatactatca    180
    25 gatggactgt gtgaaaataa accagggaag acatgctgta gaatgtgcca gtatgtgatt    240
    27 gaatgcagag tagaagcagc tggttatttt agaacgtttt acggcaaaag atttaatttt    300
    29 caggaacctg gtaaatatgt gctggctagg ggaaccaagg gtggcgattg gtctgtaacc    360
    31 ctcaccatgg agaatctaga tggacagaag ggagctgtgc tgactaagac aacactggag    420
    33 gttgcaggag acgtaataga cattactcaa gctactgcag atcctatcac agttaacgga    480
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    37 gaaataccgg gcttcaatat cacagtcatc gaattcttta aactaatcgt gattgatatt    600
    39 ctgggaggaa gatctgtgag aattgctcca gacacagcaa acaaaggact gatatctggt    660
    41 atctgtggta atctggagat gaatgacgct gatgacttta ctacagatgc agatcagctg    720
    43 gcgatccaac ccaacataaa caaagagttc gacggctgcc cattctatgg caatccttct    780
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    47 aacttctact attacactct atcctgtgcc ttcgcttact gtatgggagg agaagaaaga    900
    49 gctaaacacg tccttttcga ctatgttgag acatgcgctg cgccggaaac gagaggaacg    960
    51 tgtgttttat caggacatac tttctatgac acattcgaca aagcaagata tcaattccag   1020
    53 ggcccatgca aggagattct gatggccgca gactgttact ggaacacatg ggatgtaaag   1080
    55 gtttcacata gagacgtcga atcatacact gaggtagaga aagtaacaat caggaaacag   1140
    57 tcaactgtag tagatctcat tgtggatggc aagcaggtca aggttggagg agtggatgta   1200
    59 tctatcccgt acagctctga gaacacttcc atatactggc aggatggaga catcctgacg   1260
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    63 catatcagag atccattcga tggaaagaca tgcggcatat gtggtaacta taatcaagat   1380
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    67 tgtacagagg aacagaaacc agaagctgag cgactttgca ataatctctt tgattcttct   1500
    69 atcgacgaga aatgtaatgt ctgctacaag cctgaccgga ttgcccgatg tatgtacgag   1560
    71 tattgcctga ggggacaaca aggattttgt gaccatgctt gggagttcaa gaaagaatgc   1620
    73 tacataaaac atggagacac tctagaagta ccacctgaat gtcaaggatc cacagagccc   1680
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79 gagctgttca ccggggtggt gcccatcctg gtcgagctgg acggcgacgt aaacggccac 1860
81 aagttcagcg tgtccggcga gggcgagggc gatgccacct acggcaagct gaccctgaag 1920
83 ttcatctgca ccaccggcaa gctgcccgtg ccctggccca ccctcgtgac caccttcggc 1980
85 tacggcctgc agtgcttcgc ccgctacccc gaccacatga agcagcacga cttcttcaag 2040
87 tccgccatgc ccgaaggcta cgtccaggag cgcaccatct tcttcaagga cgacggcaac 2100
89 tacaagaccc gcgccgaggt gaagttcgag ggcgacaccc tggtgaaccg catcgagctg 2160
91 aagggcatcg acttcaagga ggacggcaac atcctggggc acaagctgga gtacaactac 2220
93 aacagccaca acgtctatat catggccgac aagcagaaga acggcatcaa ggtgaacttc 2280
95 aagatccgcc acaacatcga ggacggcagc gtgcagctcg ccgaccacta ccagcagaac 2340
97 acccccatcg gcgacggccc cgtgctgctg cccgacaacc actacctgag ctaccagtcc 2400
99 gccctgagca aagaccccaa cgagaagcgc gatcacatgg tcctgctgga gttcgtgacc 2460
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105 <211> LENGTH: 833
106 <212> TYPE: PRT
107 <213> ORGANISM: mammalian
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115 Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Pro Pro Ser Ser Thr
116 20 25 30
119 Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp
120 35 40 45
123 Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys
124 50 55 60
127 Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile
128 65 70 75 80
131 Glu Cys Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Gly Lys
132 85 90 95
135 Arg Phe Asn Phe Gln Glu Pro Gly Lys Tyr Val Leu Ala Arg Gly Thr
136 100 105 110
139 Lys Gly Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly
140 115 120 125
143 Gln Lys Gly Ala Val Leu Thr Lys Thr Thr Leu Glu Val Ala Gly Asp
144 130 135 140
147 Val Ile Asp Ile Thr Gln Ala Thr Ala Asp Pro Ile Thr Val Asn Gly
148 145 150 155 160
151 Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr
152 165 170 175
155 Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe
156 180 185 190
159 Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile
160 195 200 205
163 Ala Pro Asp Thr Ala Asn Lys Gly Leu Ile Ser Gly Ile Cys Gly Asn
164 210 215 220
167 Leu Glu Met Asn Asp Ala Asp Asp Phe Thr Thr Asp Ala Asp Gln Leu
168 225 230 235 240

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172                 245                 250                 255
175 Gly Asn Pro Ser Asp Ile Glu Tyr Cys Lys Gly Leu Met Glu Pro Tyr
176             260                 265                 270
179 Arg Ala Val Cys Arg Asn Asn Ile Asn Phe Tyr Tyr Tyr Thr Leu Ser
180         275                 280                 285
183 Cys Ala Phe Ala Tyr Cys Met Gly Gly Glu Glu Arg Ala Lys His Val
184     290                 295                 300
187 Leu Phe Asp Tyr Val Glu Thr Cys Ala Ala Pro Glu Thr Arg Gly Thr
188 305                 310                 315                 320
191 Cys Val Leu Ser Gly His Thr Phe Tyr Asp Thr Phe Asp Lys Ala Arg
192                 325                 330                 335
195 Tyr Gln Phe Gln Gly Pro Cys Lys Glu Ile Leu Met Ala Ala Asp Cys
196             340                 345                 350
199 Tyr Trp Asn Thr Trp Asp Val Lys Val Ser His Arg Asp Val Glu Ser
200         355                 360                 365
203 Tyr Thr Glu Val Glu Lys Val Thr Ile Arg Lys Gln Ser Thr Val Val
204     370                 375                 380
207 Asp Leu Ile Val Asp Gly Lys Gln Val Lys Val Gly Gly Val Asp Val
208 385                 390                 395                 400
211 Ser Ile Pro Tyr Ser Ser Glu Asn Thr Ser Ile Tyr Trp Gln Asp Gly
212                 405                 410                 415
215 Asp Ile Leu Thr Thr Ala Ile Leu Pro Glu Ala Leu Val Val Lys Phe
216             420                 425                 430
219 Asn Phe Lys Gln Leu Leu Val Val His Ile Arg Asp Pro Phe Asp Gly
220         435                 440                 445
223 Lys Thr Cys Gly Ile Cys Gly Asn Tyr Asn Gln Asp Ser Thr Asp Asp
224     450                 455                 460
227 Phe Phe Asp Ala Glu Gly Ala Cys Ala Leu Thr Pro Asn Pro Pro Gly
228 465                 470                 475                 480
231 Cys Thr Glu Glu Gln Lys Pro Glu Ala Glu Arg Leu Cys Asn Asn Leu
232                 485                 490                 495
235 Phe Asp Ser Ser Ile Asp Glu Lys Cys Asn Val Cys Tyr Lys Pro Asp
236             500                 505                 510
239 Arg Ile Ala Arg Cys Met Tyr Glu Tyr Cys Leu Arg Gly Gln Gln Gly
240         515                 520                 525
243 Phe Cys Asp His Ala Trp Glu Phe Lys Lys Glu Cys Tyr Ile Lys His
244     530                 535                 540
247 Gly Asp Thr Leu Glu Val Pro Pro Glu Cys Gln Gly Ser Thr Glu Pro
248 545                 550                 555                 560
251 Gly Leu Glu Glu Val Gly Glu Ile Glu Gln Lys Gln Leu Gln Lys Arg
252                 565                 570                 575
255 Phe Gly Gly Phe Thr Gly Ala Arg Lys Ser Ala Arg Lys Leu Ala Asn
256             580                 585                 590
259 Gln Gly Ser Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
260         595                 600                 605
263 Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
264     610                 615                 620
267 Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
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268 625                 630                 635                 640
271 Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
272                 645                 650                 655
275 Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His
276             660                 665                 670
279 Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
280         675                 680                 685
283 Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
284     690                 695                 700
287 Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
288 705                 710                 715                 720
291 Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
292                 725                 730                 735
295 Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
296             740                 745                 750
299 Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
300         755                 760                 765
303 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
304     770                 775                 780
307 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
308 785                 790                 795                 800
311 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
312                 805                 810                 815
315 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
316             820                 825                 830
319 Lys
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324 <211> LENGTH: 16
325 <212> TYPE: PRT
326 <213> ORGANISM: mammalian
328 <400> SEQUENCE: 3
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331 1               5                   10                  15
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335 <211> LENGTH: 16
336 <212> TYPE: PRT
337 <213> ORGANISM: mammalian
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346 <211> LENGTH: 14
347 <212> TYPE: PRT
348 <213> ORGANISM: mammalian
350 <400> SEQUENCE: 5
352 Ser Glu Gln Lys Gln Leu Gln Phe Gly Gly Phe Thr Gly Gly
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VERIFICATION SUMMARY DATE: 11/08/2005
PATENT APPLICATION: **US/10/537,971** TIME: 12:18:09

Input Set : **A:\PTO.RJ.txt**
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L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:10 M:283 W: Missing Blank Line separator, <160> field identifier